Fungal nucleic acids are subject to "self"-produced inhibitors and mutagens detrimental to phylogenetics and identifications

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Nucleic acids (NA) are employed for identifications, diagnoses and phylogenetics. An axiom is, "the structure of the extracted NA remains unchanged from the native molecule". Surprisingly, growth periods in reports are from 1 to 28 days in media that support enzyme-inhibitor and mutagenic secondary metabolites[1,2]. This is illogical as the structure of NA may be altered[1] and/or PCR DNA polymerases inhibited[2]. The procedures are undermined consequently and represent inadequate experimental design. There is an assumption that the growth period is simply to obtain enough biomass for extraction. Also, internal amplification controls are essential for PCR to permit detection of false negative results. Secondary metabolism requires to be understood for each taxon of taxonomic interest and protocols should reflect this comprehension. Reduced growth periods and subculturing require to be investigated, although the ratios of NA to mutagens are more important than absolute concentrations. A fundamental experiment is to test the NA of the fungi after various growth periods rather than one, as occurs presently. Otherwise, we risk eons of fungal evolutionary information within a few days growth.

References

1. Paterson, RRM, Lima, N. (2009) J Appl Microbiol, 106, 1070–1080.

2. Paterson RRM. (2007) J Appl Microbiol, 102, 1-10.